- (i) APPLICANT: Ashkenazi, Avi

 Chuntharapai, Anon

 Kim, Kyung Jin
 - (ii) TITLE OF INVENTION: Apo-2 RECEPTOR
- 15 (iii) NUMBER OF SEQUENCES: 5
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Gehentech, Inc.
 - (B) STREET: 1 DNA Way
 - (C) CITY: South San Francisco
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 94080
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: WinPatin (Genentech)
 - (vi) CURRENT APPLICATION DATA
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- 35

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- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Marschang, Diane
 - (B) REGISTRATION NUMBER: 35,600
 - (C) REFERENCE/DOCKET NUMBER: \P1101P1

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	5	(ix) TELECOMMUNICATION INFORMATION:
		(A) TELEPHONE: 650/225-5416
		(B) TELEFAX: 650/952-9881
		(C) TELEX: 910/371-7168
	4.0	
	10	(2) INFORMATION FOR SEQ ID NO:1:
		(i) SEQUENCE CHARACTERISTICS:
		(A) LENGTH: 411 amino acids
	15	(B) TYPE: Amino Acid
	13	(D) TOPOLOGY: Linear
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
11		(MI) BEGOENCE DESCRIPTION: SEQ ID NO:1:
		Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg
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		$\begin{array}{cccccccccccccccccccccccccccccccccccc$
		Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro
		20 \ 25 30
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-	25	Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val
(#		35 \ 40 45
1.1		
POL		Leu Leu Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp
NIE V	30	50 \ 55 60
		Leu Ala Pro Gla Gla Arg Ala Ala Dro Gla
Topic Control		Leu Ala Pro Gln Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser
		75
		Pro Ser Glu Gly Leu Cys Pro Pro Gly His His Ile Ser Glu Asp
	35	80 85 90
		Gly Arg Asp Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr
		$\frac{1}{100}$
	40	His Trp Asn Asp Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys Asp
		110 115 120

		5	Sei	r Gl	G1	u Vai	1 Gl:		u Se	r Pr	о Су	130		r Th	r Arg	g Ası	135
		10	Va]	l Cys	s Gl	n Cys	5 Gl:		u Gl	y Th	r Phe	e Arg		u Glı	ı Asp	Sei	Pro 150
			Glu	ı Met	: Cys	s Arg	J Lys 155		s Arg	g Th:	r Gly	7 Cys 160		o Arg	g Gly	Met	Val
		15	Lys	Val	. Gly	/ Ast) ·Cys		r Pro	o Trị	o Ser	Asp 175		e Glu	ı Cys	Val	His 180
			Lys	Glu	Ser	Gly	1)le		e Ile	e Gly	v Val	. Thr 190		. Ala	. Ala	Val	Val 195
***************************************		20	Leu	rle	Val	Ala	Val 200		· Val	. Cys	Lys	Ser 205	Leu	ı Leu	Trp	Lys	Lys 210
thomas Marcell gift ""Ye		25	Val	Leu	Pro	Tyr	Leu 215	Lys	Gly	Ile	: Cys	Ser 220	Gly	Gly	Gly	Gly	Asp 225
			Pro	Glu	Arg	Val	Asp 230	Arg	Ser	Ser	Gln	Arg 235	Pro	Gly	Ala	Glu	Asp 240
		30	Asn	Val	Leu	Asn	Glu 245	Ile	Val	Ser	Ile	Leu 250	Gln	Pro	Thr	Gln	Val 255
	N. A.		Pro	Glu	Gln	Glu	Met 260	Glu	Val	Gln	Glu	Pro 265	Ala	Glu	Pro	Thr	Gly 270
/	;	35	Val	Asn	Met	Leu	Ser 275	Pro	Gly	Glu	Ser	Glu 280	His	Leu	Leu	Glu	Pro 285
	2	10	Ala	Glu	Ala	Glu	Arg 290	Ser	Gln	Arg	Arg	Arg 295	Leu	Leu	Val		Ala 300
			Asn	Glu	Gly		Pro 305	Thr	Glu	Thr		310	dln	Cys	Phe .		Asp 315
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	5	
		Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro Leu Met Arg
		320 325 330
		330
	•	LVS Len Gly Len Met Asp Asp Cly Tle Lvs Val 31 7 7 7
	10	Lys Leu Gly Leu Met Asp Asn Glu Ile Lys Val Ala Lys Ala Glu
	10	335 340 345
		Ala Ala Gly Hts Arg Asp Thr Leu Tyr Thr Met Leu Ile Lys Trp
		\ 350 355 360
	15	Val Asn Lys Thr Gly Arg Asp Ala Ser Val His Thr Leu Leu Asp
		3,65 370 375
		\
		Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu
		200
	<u> </u>	380 385 390
	I -	Acr His Law Law Co.
		Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn
	Ti	395 \ 400 405
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3	<u></u>	Ala Asp Ser Ala Xaa Ser\
ii gi	0 0 0 0 0 1 2 5 5 7	410 411 \
411	30	(2) INFORMATION FOR SEQ ID NO:2:
thus.	<u>u</u>	
		(i) SEQUENCE CHARACTERISTICS:
4 <u>.</u>	∄ 30	(A) LENGTH: 1799 base pairs
		(B) TYPE: Nucleic Acid
1.1	Ÿ 7	(C) STRANDEDNESS: Single
*(\mathch{L}'\d	(D) TOPOLOGY: Linear
1		(b) Torollogr. Hillear
	V35	(vi) GEOLUNGE PROGRESS
	, 00	(xi) SEQUENCE DESCRIPTION: SEQ IN NO:2:
		CCCACGCGTC CGCATAAATC AGCACGCGGC CGCAAACCC CGCAATCTCT 50
	40	GCGCCCACAA AATACACCGA CGATGCCCGA TCTACTTTAA GGGCTGAAAC 100
		CCACGGGCCT GAGAGACTAT AAGAGCGTTC CCTACCGCC ATG GAA 145
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			G GGZ											
10	GLi	n Ar	g G ly		ı Asr	ı Ala	a Pro			a Ser	Gly	Ala	Arg	
10			/2					10)				15	
	AA	A AG	G CAC	, , , , , ,	י ככש	GGZ	\	ገ አርር	ב כאכ			CCA	aaa	222
			g His											
	-1	 ,	J	, <u>L</u> ,	20		LIC	ALG	, GIC	25		GIY	Ala	
15				\	\					2.3				
	AGG	CC.	r ggg	CTC	ggg	GTC	ccc	AAG	ACC	CTT	GTG	CTC	GTT	262
			o Gly											
		3 (/	\	35					40		
20	GTC	GCC	C GCG	GTC	CTG	C ∤ G	TTG	GTC	TCA	GCT	GAG	TCT	GCT	301
	Val	Ala	a Ala	Val	Leu	Leú	Leu	Val	Ser	Ala	Glu	Ser	Ala	
				45					50					
25			ACC											340
25			Thr	Gln	Gln		Leu	\Ala	Pro	Gln	Gln	Arg	Ala	
	55					60					65			
	GCC	CCA	. רא	C 7 7	770	700	шаа	,,,	~~~					
			CAA						`					379
30	7114	110	Gln 70	GIII	пуъ	Arg	ser	5er 75	Pro	ser	GIu	GIY		
			, 0					/3					80	
	TGT	CCA	CCT	GGA	CAC	CAT	ATC	TCA	GAA	GAC	GGT	AGA	СДТ	418
,	Cys	Pro	Pro	Gly	His	His	Ile	Ser	Glu	Asp	Glv	Ara	Asn	110
					85					90	1	5		
35														
	TGC	ATC	TCC	TGC	AAA	TAT	GGA	CAG	GAC	$_{\text{TAT}}$	AGC	ACT	CAC	457
	Cys	Ile	Ser	Cys	Lys	Tyr	Gly	Gln	Asp	Tyr	der	Thr	His	
		95					100				\	105		
• •											\			
10	TGG	AAT	GAC	CTC	CTT	TTC	TGC	TTG	CGC	TGC	ACC \	AGG '	TGT 4	496

115

Trp Asn Asp Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys

110

Asp Ser Gly Glu Val Glu Leu Ser Pro Cys Thr Thr AGA AAC ACA GTG TGT CAG TGC GAA GAA GGC ACC TTC CGG 574 Arg Asn Thr Val Cxs Glu Cys Glu Glu Gly Thr Phe Arg GAA GAA GAT TCT CCT AAG ATG TGC CGG AAG TGC CGC ACA 613 Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr GGG TGT CCC AGA GGG ATG GTC AAG GTC GGT GAT TGT ACA 652 Gly Cys Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr CCC TGG AGT GAC ATC GAA TGT GTC CAC AAA GAA TCA GGC 691 Pro Trp Ser Asp Ile Glu Cys Val\His Lys Glu Ser Gly

	5	Ile	١ ١				Val	GCA Ala				Leu	730
1	10			Phe				TCT Ser 205					
1	5				١ ١			ATC Ile					
2	20					1		AGA Arg					847
	.0						- 1	AAT Asn		Ile			886
iž.	5							GAG Glu					925
	0							GGT Gly 270	1				964
My 3	5							CTG Leu		1			1003
	•							CTG Leu			1		1042
41	U							CTG Leu				1	1081

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310

CTC ATG AGG AAG TTG GGC CTC ATG GAC AAT GAG ATA AAG 1159
Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile Lys
330 335 340

5 GTG GCT AAA GCT GAG GCA GCG GGC CAC AGG GAC ACC TTG 1198
Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu
345 350

TAC ACG ATG CTG ATA AAC TGG GTC AAC AAA ACC GGG CGA 1237

Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg

355

360

365

GAT GCC TCT GTC CAC ACC CTC CTG GAT GCC TTG GAG ACG 1276
Asp Ala Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr
370 375

CTG GGA GAG AGA CTT GCC AAG CAG AAG ATT GAG GAC CAC 1315 Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu Asp His 380 385 390

TTG TTG AGC TCT GGA AAG TTC ATG TAT CTA GAA GGT AAT 1354
Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn
395 400 405

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5	GCA GAC TCT GCC WTG TCC TAAGTGTG ATTCTCTTCA GGAAGTGAGA 1400
	Ala Asp Ser Ala Xaa Ser
	410 411
10	CCTTCCCTGG TTTACCTTTT TTCTGGAAAA AGCCCAACTG GACTCCAGTC 1450
	AGTAGGAAAG TGCCACAATT GTCACATGAC CGGTACTGGA AGAAACTCTC 1500
	CCATCCAACA TCACCCAGTG GATGGAACAT CCTGTAACTT TTCACTGCAC 1550
15	TTGGCATTAT TTTTATAGC TGAATGTGAT AATAAGGACA CTATGGAAAT 1600
	GTCTGGATCA TTCCGTTTGT GCGTACTTTG AGATTTGGTT TGGGATGTCA 1650
	TTGTTTTCAC AGCACTTTTT TATCCTAATG TAAATGCTTT ATTTATTTAT 1700
20	TTGGGCTACA TTGTAAGATC CATCTACAAA AAAAAAAAAA
	GGCGGCCGCG ACTCTAGAGT CGACCTGCAG AAGCTTGGCC GCCATGGCC 1799
	(2) INFORMATION FOR SEQ ID NO:3:
25	
	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 70 base pairs
	(B) TYPE: Nucleic Acid \setminus
	(C) STRANDEDNESS: Single

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

(D) TOPOLOGY: Linear

GGGAGCCGCT CATGAGGAAG TTGGGCCTCA TGGACAATGA GATAAAGGTG 50
GCTAAAGCTG AGGCAGCGGG 70

- (2) INFORMATION FOR SEQ ID NO:4: 5
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

10

ATCAGGGACT TTCCGCTGGG GACTTTCCG 29

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: Nucleic\Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGGATGGGAA GTGTGTGATA TATCCTTGAT 30

20 125 125

30